

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:09:13 ; Search time 299.73 Seconds

(without alignments)
17.597 Million cell updates/sec

Title: US-09-331-631a-3_COPY_29_73

Sequence: 1 SEFDROEYEBCKRQCMQLETF.....RCVSQCKRFPEDIDMSKYD 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_PROTOZOA:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 252 | 100.0 | 666 | 10 Q9SP15 | Q9SP15 macadamia i |
| 2 | 252 | 100.0 | 666 | 10 Q9SP14 | Q9SP14 macadamia i |
| 3 | 180 | 71.4 | 625 | 10 Q9SP13 | Q9SP13 macadamia i |
| 4 | 70.5 | 28.0 | 525 | 10 Q43358 | Q43358 theobroma c |
| 5 | 70.5 | 28.0 | 593 | 10 Q9SEW4 | Q9SEW4 juglans reg |
| 6 | 67 | 26.6 | 810 | 10 Q9ZWI3 | Q9ZWI3 cucurbita m |
| 7 | 67 | 26.6 | 1170 | 6 Q28179 | Q28179 bos taurus |
| 8 | 65 | 25.8 | 393 | 10 Q9RTPO | Q9RTPO oryza sativ |
| 9 | 64 | 25.4 | 554 | 10 Q9SG14 | Q9SG14 arabidopsis |
| 10 | 63 | 25.0 | 564 | 6 Q9TTS4 | Q9TTS4 bos taurus |
| 11 | 62.5 | 24.8 | 489 | 10 Q9SP11 | Q9SP11 glycine max |
| 12 | 62 | 24.6 | 875 | 4 Q60278 | Q60278 homo sapien |
| 13 | 62 | 24.6 | 941 | 4 Q9UKY2 | Q9UKY2 homo sapien |
| 14 | 62 | 24.6 | 941 | 4 Q9UHF8 | Q9UHF8 homo sapien |
| 15 | 62 | 24.6 | 941 | 4 Q9NZ08 | Q9NZ08 homo sapien |
| 16 | 62 | 24.6 | 1947 | 2 Q9RFX7 | Q9RFX7 stigmatalia |
| 17 | 61 | 24.2 | 554 | 10 P93719 | P93719 petunia hyb |
| 18 | 61 | 24.2 | 930 | 11 Q9J123 | Q9J123 rattus norv |
| 19 | 59.5 | 23.6 | 92 | 5 Q9VTN3 | Q9VTN3 drosophila |

| | | | | | |
|----|------|------|------|-----------|--------------------|
| 20 | 59.5 | 23.6 | 3078 | 5 Q26031 | Q26031 plasmodium |
| 21 | 59.5 | 23.6 | 3696 | 5 Q9NAB9 | Q9NAB9 caenorhabd1 |
| 22 | 59 | 23.4 | 387 | 10 Q9S9Q1 | Q9S9Q1 arabidopsis |
| 23 | 58 | 23.0 | 242 | 5 Q19919 | Q19919 caenorhabd1 |
| 24 | 58 | 23.0 | 489 | 5 Q61650 | Q61650 drosophila |
| 25 | 58 | 23.0 | 490 | 5 Q9VFN5 | Q9VFN5 drosophila |
| 26 | 58 | 23.0 | 1421 | 10 Q49539 | Q49539 arabidopsis |
| 27 | 57.5 | 22.8 | 364 | 10 Q9LIR8 | Q9LIR8 arabidopsis |
| 28 | 57 | 22.6 | 316 | 5 Q96288 | Q96288 plasmodium |
| 29 | 57 | 22.6 | 725 | 12 Q9JF74 | Q9JF74 vaccinia vi |
| 30 | 55.5 | 22.0 | 205 | 5 Q9VFA7 | Q9VFA7 plasmodium |
| 31 | 55 | 21.8 | 348 | 5 Q96290 | Q96290 plasmodium |
| 32 | 55 | 21.8 | 402 | 10 Q9ZRH8 | Q9ZRH8 oryza sativ |
| 33 | 55 | 21.8 | 623 | 10 Q9SU72 | Q9SU72 arabidopsis |
| 34 | 55 | 21.8 | 822 | 5 Q00901 | Q00901 leishmania |
| 35 | 55 | 21.8 | 4123 | 4 Q75851 | Q75851 homo sapien |
| 36 | 54.5 | 21.6 | 381 | 5 Q9VFP5 | Q9VFP5 drosophila |
| 37 | 54.5 | 21.6 | 1259 | 5 Q44971 | Q44971 caenorhabd1 |
| 38 | 54.5 | 21.6 | 2703 | 5 Q9VEG7 | Q9VEG7 drosophila |
| 39 | 54.5 | 21.6 | 2715 | 5 Q61603 | Q61603 drosophila |
| 40 | 54 | 21.4 | 314 | 10 Q9MAQ4 | Q9MAQ4 arabidopsis |
| 41 | 54 | 21.4 | 607 | 10 Q9UQC8 | Q9UQC8 pyrococcus |
| 42 | 54 | 21.4 | 880 | 1 Q9UQC8 | Q9UQC8 pyrococcus |
| 43 | 53.5 | 21.2 | 67 | 5 Q18132 | Q18132 caenorhabd1 |
| 44 | 53.5 | 21.2 | 450 | 4 Q75595 | Q75595 homo sapien |
| 45 | 53.5 | 21.2 | 450 | 4 Q9UNAB | Q9UNAB homo sapien |

ALIGNMENTS

RESULT 1
ID Q9SP15 PRELIMINARY: PRT; 666 AA.
AC Q9SP15
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-OCT-2000 (TRENBLREL. 15, Last annotation update)
DE VICILIN PRECURSOR.
GN AMP2.
OS Macadamia integrifolia (Macadamia nut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Eudicotyledons; Proteaceae; Macadamia.
OX NCBI_Taxid=60698;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=NUC KERNEL;
RA Marcus J.P., Coulter K.C., Green J.L., Manners J.M.;
RT "A family of antimicrobial peptides is produced by processing of a 7S
RT globulin protein in Macadamia integrifolia kernels.";
DR EMBL: AF161883; AAD54244.1; -
DR HSSP: P02853; 2PIL.
DR INTERPRO: IPR001113; -
DR PRAM: PR00546; Seedstore_7s; 1.
SQ SEQUENCE 666 AA; 78217 MW; C752B884B2DF0224 CRC64;

Query Match 100.0%; Score 252; DB 10; Length 666;
Best local similarity 100.0%; Pred. No. 5.9e-24;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEFDROEYEBCKRQCMQLETSQMRVSCQCKRFPEDIDMSKYD 45
DB 29 SEFDROEYEBCKRQCMQLETSQMRVSCQCKRFPEDIDMSKYD 73
RESULT 2
ID Q9SP14 PRELIMINARY: PRT; 666 AA.
AC Q9SP14
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)

DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE VICILIN PRECURSOR.
GN AMP2.
OS Macadamia integrifolia (Macadamia nut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
ON NCBI_TaxID=60698;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=NUT KERNEL;
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;
RT "A family of antimicrobial peptides is produced by processing of a 7S
RT globulin protein in Macadamia integrifolia.";
RL Plant J. 0:0-0(1999).
DR EMBL; AF161884; AAD54245.1; -.
DR HSSP; P02853; 2PHL.
DR INTERPRO: IPR001113; -.
DR PFAM; PF00546; Seedstore_7s; 1.
SQ SEQUENCE 666 AA; 78243 MW; 0ECNA22F8710F8A7B CRC64;

Query Match 100.0%; Score 252; DB 10; Length 666;
Best Local Similarity 100.0%; Pred. No. 5,9e-24;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEFDROEYECRQCMQLETSGOMRCVSCDCKRFEDIDMSKYD 45
DB 29 SEFDROEYECRQCMQLETSGOMRCVSCDCKRFEDIDMSKYD 73

RESULT 3
Q9SPJ3 PRELIMINARY: PRT; 625 AA.
AC Q9SPJ3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 13, Last annotation update)
DE VICILIN PRECURSOR (FRAGMENT).
GN AMP2.
OS Macadamia integrifolia (Macadamia nut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
ON NCBI_TaxID=60698;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=NUT KERNEL;
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;
RT "A family of antimicrobial peptides is produced by processing of a 7S
RT globulin protein in Macadamia integrifolia.";
RL Plant J. 0:0-0(1999).
DR EMBL; AF161885; AAD54246.1; -.
DR HSSP; P02853; 2PHL.
DR INTERPRO: IPR001113; -.
DR PFAM; PF00546; Seedstore_7s; 1.
FT NON_TER 1
SQ SEQUENCE 625 AA; 73586 MW; 415808A89D370296 CRC64;

Query Match 71.4%; Score 180; DB 10; Length 625;
Best Local Similarity 100.0%; Pred. No. 6,8e-15;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 QCMQLETSGOMRCVSCDCKRFEDIDMSKYD 45
DB 1 QCMQLETSGOMRCVSCDCKRFEDIDMSKYD 32

RESULT 4
ID 043358 PRELIMINARY: PRT; 525 AA.
AC 043358;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE VICILIN PRECURSOR.
GN CSV.
OS Theobroma cacao (Cacao).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Malvales; Malvaceae; Theobroma.
ON NCBI_TaxID=3641;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAVES;
RA MEDLINE:9228309; PubMed=1600151;
RA McHenry L., Fritz P.O.;
RT "Comparison of the structure and nucleotide sequences of vicilin genes
RT of cocoa and cotton raise questions about vicilin evolution.";
RL Plant Mol. Biol. 18:1173-1176(1992).
DR EMBL; X62625; CAA44493.1; -.
DR EMBL; X62626; CAA44494.1; -.
DR HSSP; P02853; 2PHL.
DR MENDEL; 30919; Thecc;1188;30919.
DR INTERPRO: IPR001113; -.
DR PFAM; PF00546; Seedstore_7s; 1.
DR PRODOM; PD081059; -. 1.
KW Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 525 VICILIN.
SQ SEQUENCE 525 AA; 60798 MW; 19114CD5C248905D CRC64;

Query Match 28.0%; Score 70.5; DB 10; Length 525;
Best Local Similarity 32.4%; Pred. No. 0.39;
Matches 11; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

QY 5 ROEYECRQCMQLETSGOMRCVSCDCKRFEE 37
DB 39 ROEYECRQCMQLETSGOMRCVSCDCKRFEE 72

RESULT 5
Q9SEW4 PRELIMINARY: PRT; 593 AA.
AC Q9SEW4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE VICILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).
OS Juglans regia (English walnut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fagales; Juglandaceae; Juglans.
ON NCBI_TaxID=51240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SUNLAND; TISSUE=SONATIC EMBRIO LINE;
RA Teuber S.S., Jarvis K.C., Peterson W.R., Dandekar A.M., Ansari A.A.;
RT "Identification and cloning of a cDNA encoding a vicilin-like protein,
RT Jug r 2, from English walnut kernel (Juglans regia): a major food
RT allergen.";
RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF066055; AAF18269.1; -.
DR HSSP; P02853; 2PHL.
DR INTERPRO: IPR001113; -.
DR PFAM; PF00546; Seedstore_7s; 1.
FT NON_TER 1
SQ SEQUENCE 593 AA; 69990 MW; 9BA127E19B18C0D8 CRC64;

Query Match 28.0%; Score 70.5; DB 10; Length 593;
Best Local Similarity 29.4%; Pred. No. 0.44;
Matches 10; Conservative 15; Mismatches 8; Indels 1; Gaps 1;
QY 5 ROEYECRQCMQLETSGOMRCVSCDCKRFEE 37
DB 39 ROEYECRQCMQLETSGOMRCVSCDCKRFEE 72

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Db      120  GQYHYHCRCRCOIQEQSPERQRCQRCRCRQYKE 153

RESULT# 6
Q9ZWT3 PRELIMINARY: PRT: 810 AA.
ID Q9ZWI3
AC Q9ZWI3:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE PV100.
OS Cucurbita maxima (Pumpkin) (Winter squash).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicot; Rosidae; eurosids I;
OC Cucurbitales; Cucurbitaceae; Cucurbita.
OX NCBI_TaxID=3661;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=KUBOKAWA AMAKURI NANKIN; TISSUE=COTYLEDON;
RX MEDLINE=99107919; PubMed=9891029;
RA Yamada K., Shimada T., Kondo M., Nishimura M., Hata-Nishimura I.;
RT "Multiple functional proteins are produced by cleaving Asn-Gln bonds
RT of a single precursor by vacuolar processing enzyme.";
RL J. Biol. Chem. 274:2563-2570(1999).
DR EMBL: AB019195; BAA34056.1; -.
DR HSSP: P02853; 2PHL.
DR INTERPRO: IPR001113; -.
DR Pfam: PF00546; Seedstore_7s; 1.
DR PRODOM: PD081059; -. 1.
SQ SEQUENCE 810 AA; 97314 MW; AB29A3F7542266AB CRC64;

Query Match 26.6%; Score 67; DB 10; Length 810;
Best Local Similarity 34.1%; Pred. NO. 1.6;
Matches 15; Conservative 6; Mismatches 15; Indels 8; Gaps 2

QY 5 ROYIECKRCQMOLETS-GQMRVCYSQCDKRF-----EDID 40
Db 75 RAEEVFCRLRCQVARGVEQQKCEQVCERLRERERQGRGQVD 118
I I I I : : I : I : I : I
I I I I : : I : I : I : I
I I I I : : I : I : I : I

RESULT 7
Q28179 PRELIMINARY: PRT: 1170 AA.
ID Q28179
AC Q28179;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE THROMBOSPONDIN 1.
DE TSP-1.
GN Bos taurus (Bovine).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=HOLSTEIN; TISSUE=ANTERIOR TOOTH;
RX MEDLINE=98173773; PubMed=9507054;
RA Ueno A., Yamashita K., Nagata T., Tsurumi C., Miwa Y., Kitamura S.,
RA Inoue H.;
RT "cDNA cloning of bovine thrombospondin 1 and its expression in
RT odontoblasts and predentin.";
RL Biochim. Biophys. Acta 1382:17-22(1998).
RN 12
RP SEQUENCE OF 1-18 FROM N.A.
RC TISSUE=AORTIC ENDOTHELIUM;
RX Zatar R.S., Moll Y.D., Womack J.F., Walz D.A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB005287; BAA2115.1; -.
DR EMBL: X87619; CAA60951.1; -.
DR HSSP: P35553; IEMN.
DR INTERPRO: IPR000561; -.

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| | | | |
|--|---|---|--------------|
| DR | INTERPRO: | IPR000884; | - |
| DR | INTERPRO: | IPR001007; | - |
| DR | INTERPRO: | IPR001791; | - |
| DR | INTERPRO: | IPR001881; | - |
| DR | INTERPRO: | IPR002465; | - |
| DR | INTERPRO: | IPR003129; | - |
| DR | PFAM: | PF000008; EGF_2. | - |
| DR | PFAM: | PF000090; tSP_L1; 3. | - |
| DR | PFAM: | PF000093; wgc; 1. | - |
| DR | PFAM: | PF02210; TSPN; 1. | - |
| DR | PROSITE: | PS003340; RECEPTOR_CYTOKINES_2; | UNKNOWN_2. |
| DR | PROSITE: | PS01186; EGF_2; 1. | - |
| DR | PROSITE: | PS01208; VMEC; 1. | - |
| SQ | SEQUENCE | 1170 AA; 129533 MW; 0DD6ADFE3EFA031A CRC64; | |
| OY | 13 ROCMOLE---- | TSGOMRRC-VSCGDKRFEEIDMSKY 44 | |
| Dd | 404 RSCDSLNNRCBESSVOTRTCHIQECDKRKFGDGMGSHW 441 | | |
| RESULT | 8 | | |
| ID | O9ZTP0 | PRELIMINARY; | PRT; 393 AA. |
| AC | O9ZTP0. | | |
| DT | 01-MAY-1999 | (TREMBLrel. 10, Created) | |
| DT | 01-MAY-1999 | (TREMBLrel. 10, Last sequence update) | |
| DE | 01-MAY-1999 | (TREMBLrel. 10, Last annotation update) | |
| DE | HYPOTHETICAL. 45.3 KDA PROTEIN. | | |
| GN | OSE705. | | |
| OS | Oryza sativa (Rice) | | |
| OC | Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; | | |
| CC | Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza. | | |
| OX | NCBI_TaxID=4530; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | STRAIN=LONELLO; | | |
| RA | Chen P.W., Chen L.J.; | | |
| RL | Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases. | | |
| DR | EMBL; AF049348; AAD02494.1; -. | | |
| KW | Hypothetical protein. | | |
| SQ | SEQUENCE 393 AA; 45258 MW; DBD01934BA2FE9E5 CRC64; | | |
| OY | 5 ROYECKRCQM--OLETSGOMRRCVSQCDDRFEEDID 40 | | |
| Dd | 37 KEELRWCKKKGCCRMENAGODQRQLRECEBCQCLNQGEDDD 74 | | |
| Query Match | | 25.8%; Score 65; DB 10; Length 393; | |
| Best Local Similarity | | 36.8%; Pred. No. 1.5; | |
| Matches 14; Conservative 7; Mismatches 15; Indels 2; Gaps 14 | | | |
| RESULT | 9 | | |
| ID | O9SG14 | PRELIMINARY; | PRT; 554 AA. |
| AC | O9SG14. | | |
| DT | 01-MAY-2000 | (TREMBLrel. 13, Created) | |
| DT | 01-MAY-2000 | (TREMBLrel. 13, Last sequence update) | |
| DE | 01-OCT-2000 | (TREMBLrel. 15, Last annotation update) | |
| DE | PURATIVE GTPASE ACTIVATOR PROTEIN OF RAB-LIKE SMALL GTPASES (GTPASE | | |
| DE | ACTIVATING-LIKE PROTEIN). | | |
| GN | TIG12.5 OR FZK15.210. | | |
| OS | Arabidopsis thaliana (Mouse-ear cress). | | |
| OC | Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; | | |
| CC | Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; | | |
| CC | Brassicales; Brassicaceae; Arabidopsis. | | |
| OX | NCBI_TaxID=3702; | | |
| RN | [1] | | |

RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
RA Roming C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome 1 BAC TIG12 genomic sequence."
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A.
RA Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M.,
RA Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
RN [13]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AC012329; AAF16581.1; -;
DR EMBL: AL132956; CAB66414.1; -;
DR INTERPRO: IPR000195; -;
DR PFAM: PF00566; TBC; 1;
SQ SEQUENCE 554 AA; 63583 MW; 430BE1FCF1D8901C CRC64;

Query Match 25.4%; Score 64; DB 10; Length 554;
Best Local Similarity 28.2%; Pred. No. 2.7;
Matches 11; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

OY 5 ROYECKRQCMOLETSGQMRRCVSGCDKRFEDIDMSK 43
DB 148 RKEVRLRQCKRLOKHNNGTRLNGSETIODEYDMPR 166

RESULT 10
O9TTS4 PRELIMINARY: PRT; 564 AA.
AC O9TTS4:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE SCO-SPONDIN (FRAGMENT).
GN SCO-SPONDIN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SUBCOMMISSURAL ORGAN;
RA Gobron S., Creveaux I., Monnerie H., El Bilar F., Didier R.,
RA Herbet A., Meinzel R., Bamdad M., Dastugue B., Meinzel A.;
RT "Characterization of cattle SCO-spondin glycoprotein."
RL Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ131107; CAB53760.1; -;
DR INTERPRO: IPR001846; -;
DR INTERPRO: IPR002919; -;
DR PFAM: PF00094; vwd; 1.
DR PFAM: PF01826; TIL; 2.
FT NON_TER 1
FT NON_TER 564
SQ SEQUENCE 564 AA; 60337 MW; 2E22DA242F9BBE7C CRC64;

Query Match 25.0%; Score 63; DB 6; Length 564;
Best Local Similarity 38.7%; Pred. No. 3.7;
Matches 12; Conservative 6; Mismatches 9; Indels 4; Gaps 1;

OY 6 OEYEE---CKRQCMOLETSGQMRRCVSGCD 32
DB 480 GEYECAPACDRNCGEPDCEGLDNCVACN 510

RESULT 11

O9SP11 PRELIMINARY: PRT; 489 AA.
AC O9SP11:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE SUCROSE BINDING PROTEIN HOMOLOG S-64.
GN SBP.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RA Pedra J.H.F., Delu-Filho N., Pirovani C.P., Contim L.S., Dewey R.E.,
RA Otonari W.C., Fontes E.P.B.;
RT "Antisense and sense expression of a sucrose binding protein homologue
RT gene from soybean in transgenic tobacco affects plant growth and
RT carbohydrate partitioning in leaves."
RL Plant Sci. 0:0-0(1999).
DR EMBL: AF191299; AAF05723.1; -;
DR HSP: P02853; 2PHL.
DR INTERPRO: IPR001113; -;
DR PFAM: PF00546; Seedstore-7s; 1.
SQ SEQUENCE 489 AA; 55834 MW; 9BBC0D45EDECECD2 CRC64;

Query Match 24.8%; Score 62.5; DB 10; Length 489;
Best Local Similarity 36.6%; Pred. No. 3.7;
Matches 15; Conservative 3; Mismatches 14; Indels 9; Gaps 2;

OY 7 EYECKRQCMOLE-TSGQMRRCVSGCD-----KRFED 38
DB 38 ELVTCCKHCCQORQYTESDKRTCLQCCDSMKQREKQVEE 78

RESULT 12
O60278 PRELIMINARY: PRT; 875 AA.
AC O60278:
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE KIAA0525 PROTEIN (FRAGMENT).
GN KIAA0525.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=98290545; PubMed=9628581;
RA Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,
RA Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. IX.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro."
RL DNA Res. 5:31-39(1998)
DR EMBL: AB011097; BAA25451.1; -;
DR MEROPS: M01.018; -;
DR INTERPRO: IPR000130; -;
DR INTERPRO: IPR001930; -;
DR PFAM: PF01433; Peptidase_M1; 1.
DR PRINTS: PR00756; ALADIPYASE.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 875
SQ SEQUENCE 875 AA; 99522 MW; C31A77DE516DEAFE CRC64;

Query Match 24.6%; Score 62; DB 4; Length 875;
Best Local Similarity 37.8%; Pred. No. 7.6;

Matches 14; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 5 ROYEBCRQCMQLETSQGMRCVSCDCKRFEEDIDW 41
 | | | | | : : | | | : | : | |
 Db 812 RTRLEEVKGFSSLKENGSQLRCVQOTIETIENIGW 848

RESULT 13

Q9UKY2 PRELIMINARY; PRT; 941 AA.

AC Q9UKY2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE ADIPOCYTE-DERIVED LEUCINE AMINOPEPTIDASE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RX MEDLINE=99238715; PubMed=10220586;
 RA Hattori A., Matsunoto H., Mizutani S., Tsujimoto M.;
 RT "Molecular cloning of adipocyte-derived leucine aminopeptidase highly
 related to placental leucine aminopeptidase/oxytocinase."
 RL J. Biochem. 125:931-938(1999).
 DR EMBL; AF106037; AAF07395.1; -;
 DR INTERPRO: IPR001930; -;
 DR PFAM: PF01433; Peptidase_M1; 1.
 DR PRINTS: PR00756; ALADIPITASE.
 DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
 KW Aminopeptidase.
 SQ SEQUENCE 941 AA; 107187 MW; 46BEF97CF78DEBCL CRC64;

Query Match 24.6%; Score 62; DB 4; Length 941;
 Best Local Similarity 37.8%; Pred. No. 8.1;
 Matches 14; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 5 ROYEBCRQCMQLETSQGMRCVSCDCKRFEEDIDW 41
 | | | | | : : | | | : | : | |
 Db 885 RTRLEEVKGFSSLKENGSQLRCVQOTIETIENIGW 921

RESULT 14

Q9UHF8 PRELIMINARY; PRT; 941 AA.

AC Q9UHF8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE AMINOPEPTIDASE PILS.
 GN APPLIS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schomburg L.;
 RT "Molecular characterization of human aminopeptidase PILS.";
 RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF183569; AAF20384.1; -;
 DR INTERPRO: IPR000130; -;
 DR INTERPRO: IPR001930; -;
 DR PFAM: PF01433; Peptidase_M1; 1.
 DR PRINTS: PR00756; ALADIPITASE.
 DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
 KW Aminopeptidase.
 SQ SEQUENCE 941 AA; 107420 MW; 2ECA71F0BACBFD74 CRC64;

Query Match 24.6%; Score 62; DB 4; Length 941;
 Best Local Similarity 37.8%; Pred. No. 8.1;
 Matches 14; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 5 ROYEBCRQCMQLETSQGMRCVSCDCKRFEEDIDW 41
 | | | | | : : | | | : | : | |
 Db 885 RTRLEEVKGFSSLKENGSQLRCVQOTIETIENIGW 921

RESULT 15

Q9NZ08 PRELIMINARY; PRT; 941 AA.

AC Q9NZ08;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE TYPE 1 TUMOR NECROSIS FACTOR RECEPTOR SHEDDING AMINOPEPTIDASE
 DE REGULATOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cui X., Alsaaty S., Lawrence M., Combs C.A., Rouhani F.N.,
 RA Levine S.J.;
 RT "Identification of an Aminopeptidase Regulator of Type I Tumor
 Necrosis Factor Receptor Shedding."
 RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF222340; AAF34664.1; -;
 DR RECEPTOR; Aminopeptidase.
 KW Receptor.
 SQ SEQUENCE 941 AA; 107234 MW; 22A0795C90155F04 CRC64;

Query Match 24.6%; Score 62; DB 4; Length 941;
 Best Local Similarity 37.8%; Pred. No. 8.1;
 Matches 14; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 5 ROYEBCRQCMQLETSQGMRCVSCDCKRFEEDIDW 41
 | | | | | : : | | | : | : | |
 Db 885 RTRLEEVKGFSSLKENGSQLRCVQOTIETIENIGW 921

Search completed: March 1, 2001, 16:09:13
 Job time: 1557 sec

